#8

See p. 148

```
 1   (1) GENERAL INFORMATION:
 2
 3       (i)  APPLICANTS:  Boon, Thierry, Van den Eynde, Beno t
 4
 5       (ii) TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
 6   Rejection Antigens and Uses Thereof
 7
 8       (iii) NUMBER OF SEQUENCES:  16
 9
10       (iv) CORRESPONDENCE ADDRESS:
11           (A) ADDRESSEE:  Felfe & Lynch
12           (B) STREET:  805 Third Avenue
13           (C) CITY:  New York City
14           (D) STATE:  New York
15           (F) ZIP:  10022
16
17       (v) COMPUTER READABLE FORM:
18           (A) MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
19           (B) COMPUTER:  IBM
20           (C) OPERATING SYSTEM:  PC-DOS
21           (D) SOFTWARE:  Wordperfect
22
23       (vi) CURRENT APPLICATION DATA:
24           (A) APPLICATION NUMBER:  07/807,043
25           (B) FILING DATE:  12-DECEMBER-1991
26           (C) CLASSIFICATION:
27
28       (vii) PRIOR APPLICATION DATA:
29           (A) APPLICATION NUMBER:  07/764,364
30           (B) FILING DATE:  23-SEPTEMBER-1991
31
32       (vii) PRIOR APPLICATION DATA:
33           (A) APPLICATION NUMBER: 07/728,838
34           (b) FILING DATE:  9-JULY-1991
35
36       (vii) PRIOR APPLICATION DATA:
37           (A) APPLICATION NUMBER:  07/705,702
38           (B) FILING DATE:  23-May-1991
39
40       (viii) ATTORNEY/AGENT INFORMATION:
41           (A) NAME:  Hanson, Norman D.
42           (B) REGISTRATION NUMBER:  30,946
43           (C) REFERENCE/DOCKET NUMBER:  LUD 253.3
44
45       (ix) TELECOMMUNICATION INFORMATION:
46           (A) TELEPHONE: (212) 688-9200
47           (B) TELEFAX: (212) 838-3884
48
49
50   (2) INFORMATION FOR SEQUENCE ID NO: 1:
51       (i) SEQUENCE CHARACTERISTICS:
52           (A) LENGTH:  462 base pairs
53           (B) TYPE:  nucleic acid
```

capitalize → (line 34)

(C) Strandedness: _____ ← please insert this field.
It is mandatory for each nucleic sequence.
(Insert for all 16 sequences)

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 54                  (D) TOPOLOGY:  linear
 55          (ii) MOLECULE TYPE:  genomic DNA
 56          (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 1:
 57
 58
 59
 60
 61  ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG    60
 62  ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT   120
 63  CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG   180
 64  CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC   240
 65  CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT   300
 66  AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT   360
 67  GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT   420
 68  TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                      462
 69
 70
 71  (2)   INFORMATION FOR SEQUENCE ID NO: 2:
 72          (i) SEQUENCE CHARACTERISTICS:
 73                  (A) LENGTH:  675 base pairs
 74                  (B) TYPE:  nucleic acid
 75                  (D) TOPOLOGY:  linear
 76          (ii) MOLECULE TYPE:  genomic DNA
 77          (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
 78
 79
 80  ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT     48
 81  Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
 82                  5                   10                  15
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 84  GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA     96
 85  Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
 86                  20                  25                  30
 87
 88  GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA    144
 89  Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
 90                  35                  40                  45
 91
 92  AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG    192
 93  Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
 94          50                  55                  60
 95
 96  TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC    240
 97  Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
 98  65                  70                  75                  80
 99
100  TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC    288
101  Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
102                  85                  90                  95
103
104  GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT    336
105  Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
106                  100                 105                 110
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107
108  GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG      384
109  Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
110          115                 120                 125
111
112  GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
113  Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
114      130                 135                 140
115
116  GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
117  Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
118  145                 150                 155                 160
119
120  AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC      528
121  Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
122              165                 170                 175
123
124  CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT      576
125  Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
126              180                 185                 190
127
128  GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG      624
129  Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
130          195                 200                 205
131
132  GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      672
133  Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
134  210                 215                 220                 225
135
136  TAG                                                                  675
137
138  (2)   INFORMATION FOR SEQUENCE ID NO: 3:
139          (i) SEQUENCE CHARACTERISTICS:
140              (A) LENGTH:  228 base pairs
141              (B) TYPE:  nucleic acid
142              (D) TOPOLOGY:  linear
143       (ii) MOLECULE TYPE:  genomic DNA
144       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 3:
145
146
147
148
149  GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT      60
150  TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT     120
151  TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC     180
152  ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                 228
153
154
155
156  (2)   INFORMATION FOR SEQUENCE ID NO: 4:
157          (i) SEQUENCE CHARACTERISTICS:
158              (A) LENGTH:  1365 base pairs
159              (B) TYPE:  nucleic acid
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160   (D) TOPOLOGY: linear
161   (ii) MOLECULE TYPE: genomic DNA
162   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
163
164
165
166
167   ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT   50
168   GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT   100
169   CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG   150
170   AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT   200
171   CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA   250
172   CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT   300
173   AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG   350
174   CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG   400
175   CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT   450
176   ACCCTTTGTG CC   462
177   ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA   504
178   GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG   546
179   TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC   588
180   TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC   630
181   ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC   672
182   TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG   714
183   GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC   756
184   GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT   798
185   GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA   840
186   GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA   882
187   GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT   924
188   GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT   966
189   TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG   1008
190   AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT   1050
191   GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG   1092
192   GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT   1134
193   TAG   1137
194   GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG   1187
195   TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA   1237
196   ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT   1287
197   CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT   1337
198   GTTAAAAATA AAAGTTTGAC TTGCATAC   1365
199
200
201
202   (2)   INFORMATION FOR SEQUENCE ID NO: 5:
203   (i) SEQUENCE CHARACTERISTICS:
204   (A) LENGTH: 4698 base pairs
205   (B) TYPE: nucleic acid
206   (D) TOPOLOGY: linear
207   (ii) MOLECULE TYPE: genomic DNA
208   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209
210
211
212   ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT   50

Patent Application US/07/807,043

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213  GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT    100
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215  AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT    200
216  CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA    250
217  CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT    300
218  AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG    350
219  CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG    400
220  CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT    450
221  ACCCTTTGTG CC                                            462
222  ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA    504
223  GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG    546
224  TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC    588
225  TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC    630
226  ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC    672
227  TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG    714
228  GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC    756
229  GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT    798
230  GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA    840
231  GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA    882
232  GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T            916
233  GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA    966
234  CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC    1016
235  TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC    1066
236  CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC    1116
237  TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC    1166
238  TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC    1216
239  TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC    1266
240  CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT    1316
241  TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT    1366
242  TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT    1416
243  CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG    1466
244  TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT    1516
245  CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT    1566
246  TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC    1616
247  TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG    1666
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251  TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC    1866
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255  TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC    2066
256  CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT    2116
257  TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT    2166
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261  TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG    2366
262  GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC    2416
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265  CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA    2566
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269  TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC    2766
270  TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC    2816
271  CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC    2866
272  ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA    2916
273  AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC    2966
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275  CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG    3066
276  CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA    3116
277  GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG    3166
278  TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA    3216
279  TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA    3266
280  GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT    3316
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282   GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT  3396
283  AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT  3438
284  ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA  3480
285  AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA  3522
286  GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC  3564
287  TTC TCA CCT TAG                                          3576
288  GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA    3626
289  GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA    3676
290  TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA    3726
291  CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT    3776
292  GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA    3826
293  GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG    3876
294  TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT    3926
295  TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG    3976
296  TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT    4026
297  CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT    4076
298  TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA    4126
299  AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA    4176
300  GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA    4226
301  GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC    4276
302  CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC    4326
303  ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT    4376
304  ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA    4426
305  AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC    4476
306  AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT    4526
307  TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA    4576
308  TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT    4626
309  GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA    4676
310  AATAAAAGTT TGACTTGCAT AC                                  4698
311
312
313  (2)   INFORMATION FOR SEQUENCE ID NO: 6:
314        (i) SEQUENCE CHARACTERISTICS:
315            (A) LENGTH:  7 amino acids
316            (B) TYPE:  amino acid
317            (D) TOPOLOGY:  linear
318        (ii) MOLECULE TYPE:  protein
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319   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
320
321
322
323
324   Leu Pro Tyr Leu Gly Trp Leu
325   5
326
327
328
329
330
331
332
333   (2)   INFORMATION FOR SEQUENCE ID NO: 7:
334   (i) SEQUENCE CHARACTERISTICS:
335   (A) LENGTH: 2418 base pairs
336   (B) TYPE: nucleic acid
337   (D) TOPOLOGY: linear
338   (ii) MOLECULE TYPE: genomic DNA
339   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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341
342
343
344   GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG   50
345   GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC   100
346   TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG   150
347   GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT   200
348   TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT   250
349   GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA   300
350   CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT   350
351   CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC   400
352   TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC   450
353   CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG   500
354   TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT   550
355   CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT   600
356   GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC   650
357   ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG   700
358   GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC   750
359   CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC   800
360   AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA   850
361   CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG   900
362   TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT   950
363   TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG   1000
364   GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA   1050
365   GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG   1100
366   TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA   1150
367   GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC   1200
368   AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG   1250
369   CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT   1300
370   GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA   1350
371   TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC   1400

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372    CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT      1450
373    ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT      1500
374    TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT      1550
375    CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC      1600
376    ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG      1650
377    CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCTCAGT AGTAGGTTTC      1700
378    TGTTCTATTG GGTGACTTGG AGATTATCT TTGTTCTCTT TTGGAATTGT       1750
379    TCAAATGTTT TTTTTAAGG GATGGTTGAA TGAACTTCAG CATCCAAGTT       1800
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381    GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG      1900
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396                (A) LENGTH:  5724 base pairs     The computer detected a
397                (B) TYPE:    nucleic acid        discrepancy. Please recount
398                (D) TOPOLOGY:  linear            the base pairs.
399          (ii)  MOLECULE TYPE:  genomic DNA
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401                (A) NAME/KEY:  MAGE-1 gene
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529       (i) SEQUENCE CHARACTERISTICS:
530           (A) LENGTH:  4157 base pairs
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Patent Application US/07/807,043

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532              (D) TOPOLOGY:  linear
533        (ii) MOLECULE TYPE:  genomic DNA
534        (ix) FEATURE:
535              (A) NAME/KEY:  MAGE-2 gene
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636                (B) TYPE:    nucleic acid
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671   (B) TYPE: nucleic acid
672   (D) TOPOLOGY: linear
673   (ii) MOLECULE TYPE: cDNA to mRNA
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692  GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC              549
693  AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC              591
694  GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT              633
695  TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA              675
696  GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG              717
697  GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG              759
698  CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA              801
699  AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG              843
700  CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG              885
701  TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG              927
702  GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT              969
703  GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA              1011
704  ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT              1053
705  GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT              1095
706  TTG AGA GAG GGG GAA GAG TGA                                          1116
707  GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT               1166
708  GCACCTTCCG GGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA                1216
709  GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG               1266
710  TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG               1316
711  TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG               1366
712  GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG               1416
713  TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA               1466
714  TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC               1516
715  GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG               1566
716  ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA               1616
717  ACCAGGATTT CCTTGACTTC TTTG                                           1640
718
719
720
721
722  (2)   INFORMATION FOR SEQUENCE ID NO: 12:
723        (i) SEQUENCE CHARACTERISTICS:
724              (A) LENGTH:  943 base pairs
725              (B) TYPE:   nucleic acid
726              (D) TOPOLOGY:  linear
727        (ii) MOLECULE TYPE:  genomic DNA
728        (ix) FEATURE:
729              (A) NAME/KEY:  MAGE-31 gene
730        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 12:
731
732
733
734  GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT               50
735  CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG               100
736  GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG               150
737  AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA               200
738  GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC               250
739  CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT               300
740  TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC               350
741  CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC               400
742  AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG               450
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743   TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC          500
744   TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCACA          550
745   CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                                580
746   ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA         622
747   GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG         664
748   CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT         706
749   TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC         748
750   GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC         790
751   CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT         832
752   GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC         874
753   CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG         916
754   GTG GCC AAG TTG GTT CAT TTT CTG CTC                             943
755
756
757
758
759   (2)   INFORMATION FOR SEQUENCE ID NO: 13:
760         (i) SEQUENCE CHARACTERISTICS:
761               (A) LENGTH:  1067 base pairs
762               (B) TYPE:   nucleic acid
763               (D) TOPOLOGY:  linear
764         (ii) MOLECULE TYPE:  cDNA to mRNA
765         (ix) FEATURE:
766               (A) NAME/KEY:  cDNA MAGE-4
767         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 13:
768
769
770
771         GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA         39
772   GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG         81
773   CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA        123
774   ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT        165
775   GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT        207
776   GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC        249
777   ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG        291
778   GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC        333
779   GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG        375
780   GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT        417
781   GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC        459
782   ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG        501
783   GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT        543
784   CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG        585
785   CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA        627
786   TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC        669
787   TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG          719
788   TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG          769
789   GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG          819
790   GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA          869
791   ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA          919
792   AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT          969
793   AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT         1019
794   TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC          1067
795
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796
797   (2)   INFORMATION FOR SEQUENCE ID NO: 14:
798         (i) SEQUENCE CHARACTERISTICS:
799             (A) LENGTH:  226 base pairs
800             (B) TYPE:  nucleic acid
801             (D) TOPOLOGY:  linear
802         (ii) MOLECULE TYPE:  genomic DNA
803         (ix) FEATURE:
804             (A) NAME/KEY:  MAGE-5 gene
805         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 14:
806
807
808
809   AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT          50
810   AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA GGCTTCTCAC         100
811   ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC         150
812   CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC                          184
813   ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA         226
814
815   (2)   INFORMATION FOR SEQUENCE ID NO: 15:
816         (i) SEQUENCE CHARACTERISTICS:
817             (A) LENGTH:  225 base pairs
818             (B) TYPE:  nucleic acid
819             (D) TOPOLOGY:  linear
820         (ii) MOLECULE TYPE:  cDNA
821         (ix) FEATURE:
822             (A) NAME/KEY:  MAGE-6 gene
823         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 15:
824
825
826
827   TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG         42
828   CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC         84
829   GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC        126
830   GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC        168
831   TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC        210
832   TGT GCC CCT GAG GAG                                            225
833
834
835
836
837
838   (2)   INFORMATION FOR SEQUENCE ID NO: 16:
839         (i) SEQUENCE CHARACTERISTICS:
840             (A) LENGTH:  166 base pairs
841             (B) TYPE:  nucleic acid
842             (D) TOPOLOGY:  linear
843         (ii) MOLECULE TYPE:  genomic DNA
844         (ix) FEATURE:
845             (A) NAME/KEY:  MAGE-7 gene
846         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 16:
847
848
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849
850   ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG        42
851   TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC.       84
852   CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC        126
853   TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A          166
854
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LINE ERROR   ORIGINAL TEXT

_OK_

24	Wrong application Serial Number	(A) APPLICATION NUMBER: 07/807,043	
34	Response Exceeds Line Limitations	(b) FILING DATE: 9-JULY-1991	
56	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
77	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 2
144	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 3
162	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 4
208	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 5
339	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 7
339	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 7
402	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 8
402	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 8
536	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 9
641	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
676	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
730	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
767	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
805	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
823	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1
846	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/807,043

MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY
STRANDEDNESS

LINE ORIGINAL TEXT   CORRECTED TEXT

LINE	ORIGINAL TEXT	CORRECTED TEXT
3	(i) APPLICANTS: Boon, Thierry, Van den	(i) APPLICANT: Boon, Thierry, Van den E
50	(2) INFORMATION FOR SEQUENCE ID NO: 1:	(2) INFORMATION FOR SEQ ID NO: 1:
71	(2) INFORMATION FOR SEQUENCE ID NO: 2:	(2) INFORMATION FOR SEQ ID NO: 2:
138	(2) INFORMATION FOR SEQUENCE ID NO: 3:	(2) INFORMATION FOR SEQ ID NO: 3:
156	(2) INFORMATION FOR SEQUENCE ID NO: 4:	(2) INFORMATION FOR SEQ ID NO: 4:
202	(2) INFORMATION FOR SEQUENCE ID NO: 5:	(2) INFORMATION FOR SEQ ID NO: 5:
313	(2) INFORMATION FOR SEQUENCE ID NO: 6:	(2) INFORMATION FOR SEQ ID NO: 6:
333	(2) INFORMATION FOR SEQUENCE ID NO: 7:	(2) INFORMATION FOR SEQ ID NO: 7:
394	(2) INFORMATION FOR SEQUENCE ID NO: 8:	(2) INFORMATION FOR SEQ ID NO: 8:
528	(2) INFORMATION FOR SEQUENCE ID NO: 9:	(2) INFORMATION FOR SEQ ID NO: 9:
633	(2) INFORMATION FOR SEQUENCE ID NO: 10:	(2) INFORMATION FOR SEQ ID NO: 10:
668	(2) INFORMATION FOR SEQUENCE ID NO: 11:	(2) INFORMATION FOR SEQ ID NO: 11:
722	(2) INFORMATION FOR SEQUENCE ID NO: 12:	(2) INFORMATION FOR SEQ ID NO: 12:
759	(2) INFORMATION FOR SEQUENCE ID NO: 13:	(2) INFORMATION FOR SEQ ID NO: 13:
797	(2) INFORMATION FOR SEQUENCE ID NO: 14:	(2) INFORMATION FOR SEQ ID NO: 14:
815	(2) INFORMATION FOR SEQUENCE ID NO: 15:	(2) INFORMATION FOR SEQ ID NO: 15:
838	(2) INFORMATION FOR SEQUENCE ID NO: 16:	(2) INFORMATION FOR SEQ ID NO: 16: